# RAW SEQUENCE LISTING ERROR REPORT
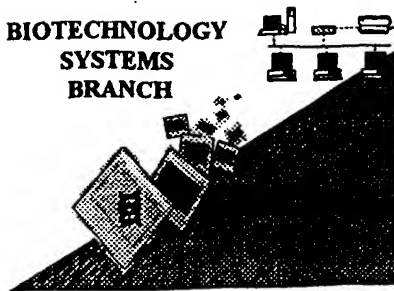
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___09/068,253___

Source: ___1653___

Date Processed by STIC: ___2/26/2001___

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TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

# Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>  <u>SUGGESTED CORRECTION</u>    SERIAL NUMBER: _09/068,253_

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

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1 _____ Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos    The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length    The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid    The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering    between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII    This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length    Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences    Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES)    (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences    Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES)    <210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's    . Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)    Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism    Sequence(s) _____ are missing this mandatory field or its response.
(NEW RULES)

12 _____ Use of <220>Feature    Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES)    Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)    (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

(J. Moezie)

RAW SEQUENCE LISTING
PATENT APPLICATION:  US/09/068,253

DATE: 02/26/2001
TIME: 16:41:00

Does Not Comply
Corrected Diskette Needed

Input Set : A:\19624051.app
Output Set: N:\CRF3\02262001\I068253.raw

pp 1-2

```
  3 <110> APPLICANT: SHIMURA, Takesada
  4         TORIYAMA, Satsuki
  6 <120> TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION
  8 <130> FILE REFERENCE: 146.1286
 10 <140> CURRENT APPLICATION NUMBER: 09/068,253
 11 <141> CURRENT FILING DATE: 1998-06-09
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP96/03333
 14 <151> PRIOR FILING DATE: 1996-11-14
 16 <150> PRIOR APPLICATION NUMBER: JP 7/322402
 17 <151> PRIOR FILING DATE: 1995-11-17
 19 <160> NUMBER OF SEQ ID NOS: 4
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 357
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)..(357)
 31 <223> OTHER INFORMATION: Relevant amino acid residues in SEQ ID NO: 1 from
 32         1 to 119 in WO 95/04819
 34 <300> PUBLICATION INFORMATION:
 35 <301> AUTHORs: HOTTEN, Gertrud
 36         NEIDHARDT, Helge
 37         PAULISTA, Michael
 38 <302> TITLE: NEW GROWTH/DIFFERENTIATION FACTOR OF THE TGF-BETA
 39         FAMILY
 40 <310> PATENT DOCUMENT NUMBER: WO 95/04819
 41 <311> PATENT FILING DATE: 1995-02-16
 42 <313> RELEVANT RESIDUES: 1 TO 119
 44 <400> SEQUENCE: 1
 45 cca ctg gcc act cgc cag ggc aag cga ccc agc aag aac ctt aag gct   48
 46 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
 47  1               5                  10                  15
 49 cgc tgc agt cgg aag gca ctg cat gtc aac ttc aag gac atg ggc tgg   96
 50 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
 51             20                  25                  30
 53 gac gac tgg atc atc gca ccc ctt gag tac gag gct ttc cac tgc gag  144
 54 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
 55         35                  40                  45
 57 ggg ctg tgc gag ttc cca ttg cgc tcc cac ctg gag ccc acg aat cat  192
 58 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
 59         50                  55                  60
 61 gca gtc atc cag acc ctg atg aac tcc atg gac ccc gag tcc aca cca  240
 62 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
 63  65                  70                  75                  80
 65 ccc acc tgc tgt gtg ccc acg cga ctg agt ccc atc agc atc ctc ttc  288
```

W--> <span>give the serial number of the filed application, not the issued patent number (see 1.823 of new Sequence Rules)</span>

RAW SEQUENCE LISTING          DATE: 02/26/2001
PATENT APPLICATION:  US/09/068,253     TIME: 16:41:00

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Input Set : A:\19624051.app
Output Set: N:\CRF3\02262001\I068253.raw

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```
66 Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
67             85                  90              95
69 att gac tct gcc aac aac gtg gtg tat aag cag tat gag gac atg gtc    336
70 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
71             100                 105             110
73 gtg gag tcg tgt ggc tgc agg                                        357
74 Val Glu Ser Cys Gly Cys Arg
75             115
78 <210> SEQ ID NO: 2
79 <211> LENGTH: 119
80 <212> TYPE: PRT
81 <213> ORGANISM: Homo sapiens
83 <400> SEQUENCE: 2
84 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
85   1           5               10              15
87 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
88             20                  25              30
90 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
91             35                  40              45
93 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
94       50                  55                  60
96 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
97 65                  70                  75                  80
99 Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
100            85                  90                  95
102 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
103            100                 105             110
105 Val Glu Ser Cys Gly Cys Arg
106            115
110 <210> SEQ ID NO: 3
111 <211> LENGTH: 27
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Description of Artificial Sequence:
117       oligonucleotide
119 <220> FEATURE:
120 <221> NAME/KEY: misc_feature
121 <222> LOCATION: (1)..(27)
122 <223> OTHER INFORMATION: PCR forward primer for isolating mature-type MP52
124 <400> SEQUENCE: 3
125 ataatgccac tagcaactcg tcagggc                                      27
128 <210> SEQ ID NO: 4
129 <211> LENGTH: 26
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Description of Artificial Sequence:
135       oligonucleotide
```

*invalid response – give source of genetic material – (see circled portion of item 12 on Error Summary sheet)*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/068,253

DATE: 02/26/2001
TIME: 16:41:00

Input Set : A:\19624051.app
Output Set: N:\CRF3\02262001\I068253.raw

```
137 <220> FEATURE:
138 <221> NAME/KEY: misc_feature
139 <222> LOCATION: Complement((1)..(26))
140 <223> OTHER INFORMATION: PCR reverse primer for isolating mature-type MP52
142 <400> SEQUENCE: 4
143 cgtcgactac ctgcagccac acgact                                    26
```

VERIFICATION SUMMARY                    DATE: 02/26/2001
PATENT APPLICATION:  US/09/068,253      TIME: 16:41:01

Input Set : A:\19624051.app
Output Set: N:\CRF3\02262001\I068253.raw

L:40 M:256 W: Invalid Numeric Header Field, Wrong PATENT DOCUMENT NUMBER:US NN/NNN,NNN